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## SEQUENCE LISTING

<110> International Flower Developments Pty. Ltd.  
 Brugliera, Filippa (US only)  
 Tanaka, Yoshikazu (US only)  
 Mason, John (US only)

<120> Genetic Sequences and Uses Therefor

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<150> AU 2002951088

<151> 2002-08-30

<150> AU 2002952835

<151> 2002-09-16

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Leu Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Thr Arg Met  
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Gly Met Val Leu Val Ser Tyr Ile Leu Gly Thr Leu Val His Ser Phe  
450 455 460

Asp Trp Lys Leu Pro Asn Gly Val Ser Glu Ile Asn Met Asp Glu Ser  
465 470 475 480

Phe Gly Leu Ala Leu Gln Lys Ala Val Pro Leu Ser Ala Thr Val Ser  
485 490 495

Pro Arg Leu Ala Pro Ser Ala Tyr Val Ile  
500 505

<210> 11  
<211> 1782  
<212> DNA  
<213> viola

<220>  
<221> misc feature  
<222> (307)..(307)  
<223> n = any nucleotide

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cggttggccc ttggtggggc ceetccctct cctaggcgcc atgcctcagc tcgcactagc 180  
caaaactcgt aagaagtatg gtccgatcat gcaacctaaa atgggcacgt ggcacatggt 240  
ggtcgcgtcc acccccagat cggctcgagc ctctctcaaa acgctagacc tcaacttctc 300  
caaccgncca cccaacgcgg ggcgctccca cctagcgtag ggcgcgcagg acttagtctt 360  
cgccaagtac ggtccgaggt ggaagacttt aagaaaattg agcaacctcc acatgctagg 420

- 15 -

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cgggaaggcg ttggatgatt gggcaaattgt gagggtoacc gagctaggcc acatgcttaa 480
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tgaaaataat gaatcggaaa aaaaaaaaaa aaaaaaaaaa aa 1782

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<210> 12  
<211> 506  
<212> PRT  
<213> viola

<400> 12

Met Ala Ile Leu Val Thr Asp Phe Val Val Ala Ala Ile Ile Phe Leu  
1 5 10 15

- 16 -

Ile Thr Arg Phe Leu Val Arg Ser Leu Phe Lys Lys Pro Thr Arg Pro  
20 25 30

Leu Pro Pro Gly Pro Leu Gly Trp Pro Leu Val Gly Ala Leu Pro Leu  
35 40 45

Leu Gly Ala Met Pro His Val Ala Leu Ala Lys Leu Ala Lys Lys Tyr  
50 55 60

Gly Pro Ile Met His Leu Lys Met Gly Thr Cys Asp Met Val Val Ala  
65 70 75 80

Ser Thr Pro Glu Ser Ala Arg Ala Phe Leu Lys Thr Leu Asp Leu Asn  
85 90 95

Phe Ser Asn Arg Pro Pro Asn Ala Gly Ala Ser His Leu Ala Tyr Gly  
100 105 110

Ala Gln Asp Leu Val Phe Ala Lys Tyr Gly Pro Arg Trp Lys Thr Leu  
115 120 125

Arg Lys Leu Ser Asn Leu His Met Leu Gly Gly Lys Ala Leu Asp Asp  
130 135 140

Trp Ala Asn Val Arg Val Thr Glu Leu Gly His Met Leu Lys Ala Met  
145 150 155 160

Cys Glu Ala Ser Arg Cys Gly Glu Pro Val Val Leu Ala Glu Met Leu  
165 170 175

Thr Tyr Ala Met Ala Asn Met Ile Gly Gln Val Ile Leu Ser Arg Arg  
180 185 190

Val Phe Val Thr Lys Gly Thr Glu Ser Asn Glu Phe Lys Asp Met Val  
195 200 205

Val Glu Leu Met Thr Ser Ala Gly Tyr Phe Asn Ile Gly Asp Phe Ile  
210 215 220

Pro Ser Ile Ala Trp Met Asp Leu Gln Gly Ile Glu Arg Gly Met Lys  
225 230 235 240



- 17 -

Lys Leu His Thr Lys Phe Asp Val Leu Leu Thr Lys Met Val Lys Glu  
 245 250 255

His Arg Ala Thr Ser His Glu Arg Lys Gly Lys Ala Asp Phe Leu Asp  
 260 265 270

Val Leu Leu Glu Glu Cys Asp Asn Thr Asn Gly Glu Lys Leu Ser Ile  
 275 280 285

Thr Asn Ile Lys Ala Val Leu Leu Asn Leu Phe Thr Ala Gly Thr Asp  
 290 295 300

Thr Ser Ser Ser Ile Ile Glu Trp Ala Leu Thr Glu Met Ile Lys Asn  
 305 310 315 320

Pro Thr Ile Leu Lys Lys Ala Gln Glu Glu Met Asp Arg Val Ile Gly  
 325 330 335

Arg Asp Arg Arg Leu Leu Glu Ser Asp Ile Ser Ser Leu Pro Tyr Leu  
 340 345 350

Gln Ala Ile Ala Lys Glu Thr Tyr Arg Lys His Pro Ser Thr Pro Leu  
 355 360 365

Asn Leu Pro Arg Ile Ala Ile Gln Ala Cys Glu Val Asp Gly Tyr Tyr  
 370 375 380

Ile Pro Lys Asp Ala Arg Leu Ser Val Asn Ile Trp Ala Ile Gly Arg  
 385 390 395 400

Asp Pro Asn Val Trp Glu Asn Pro Leu Glu Phe Leu Pro Glu Arg Phe  
 405 410 415

Leu Ser Glu Glu Asn Gly Lys Ile Asn Pro Gly Gly Asn Asp Phe Lys  
 420 425 430

Leu Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Thr Arg Met  
 435 440 445

Gly Met Val Leu Val Ser Tyr Ile Leu Gly Thr Leu Val His Ser Phe  
 450 455 460

- 18 -

Asp Trp Lys Leu Pro Asn Gly Val Ala Glu Leu Asn Met Asp Glu Ser  
 465 470 475 480

Phe Gly Leu Ala Leu Gln Lys Ala Val Pro Leu Ser Ala Leu Val Ser  
 485 490 495

Pro Arg Leu Ala Ser Asn Pro Tyr Ala Thr  
 500 505

<210> 13  
 <211> 1659  
 <212> DNA  
 <213> salvia

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 ggggcccagg ggctttctag tgggtgggctc ccttcccttg ctgggcgaca tgccacatgt 180  
 cgccctagca aaaatggcca aaacttaagg ccgatcatg tacttgaaaa tgggcacagt 240  
 cggcatgggc gtggcggtcca cgccagacgc ggcgcggggc ttcttaaaaa cccacgacgc 300  
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- 19 -

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<210> 14
<211> 520
<212> PRT
<213> salvia

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<400> 14

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Gly Thr Ser Met Glu Ala Gln Glu Asn Met Leu Leu Ile Ala Arg Ala
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Leu Val Val Ala Ser Leu Leu Tyr Ile Leu Ile Arg Met Phe Ile Ser
20           25           30

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```

Lys Leu Ser Thr Thr Gly His Pro Leu Pro Pro Gly Pro Arg Gly Phe
35           40           45

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```

Leu Val Val Gly Ser Leu Pro Leu Leu Gly Asp Met Pro His Val Ala
50           55           60

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Leu Ala Lys Met Ala Lys Thr Tyr Gly Pro Ile Met Tyr Leu Lys Met
65           70           75           80

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```

Gly Thr Val Gly Met Val Val Ala Ser Thr Pro Asp Ala Ala Arg Ala
85           90           95

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```

Phe Leu Lys Thr His Asp Ala Asn Phe Ser Asn Arg Pro Val Asn Ala
100          105          110

```

```

Gly Ala Thr Ile Leu Ala Tyr Asn Ala Gln Asp Met Val Phe Ala Pro
115          120          125

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- 20 -

Tyr Gly Pro Lys Trp Arg Leu Leu Arg Lys Leu Ser Ser Leu His Met  
 130 135 140

Leu Gly Ser Lys Ala Leu Glu Glu Trp Ala Asp Val Arg Thr Ser Glu  
 145 150 155 160

Val Gly His Met Leu Ala Ala Met His Glu Ala Ser Arg Leu Gly Glu  
 165 170 175

Ala Val Gly Leu Pro Glu Met Leu Val Tyr Ala Thr Ala Asn Met Ile  
 180 185 190

Gly Gln Val Ile Leu Ser Arg Arg Val Phe Val Thr Lys Gly Lys Glu  
 195 200 205

Met Asn Glu Phe Lys Glu Met Val Val Glu Leu Met Thr Thr Ala Gly  
 210 215 220

Tyr Phe Asn Ile Gly Asp Phe Ile Pro Trp Leu Ala Trp Met Asp Leu  
 225 230 235 240

Gln Gly Ile Glu Arg Gly Met Lys Lys Leu His Lys Lys Trp Asp Arg  
 245 250 255

Leu Ile Gly Lys Met Leu Asp Asp Arg Leu Lys Ser Thr Tyr Lys Arg  
 260 265 270

Asn Asp Lys Pro Asp Leu Leu Asp Ser Leu Leu Ala Asn His Asp Asp  
 275 280 285

Glu Ser Lys Asp Asp Asp Glu Asp Cys Lys Leu Thr Thr Thr Asn Ile  
 290 295 300

Lys Ala Leu Leu Leu Asn Leu Phe Thr Ala Gly Thr Asp Thr Ser Ser  
 305 310 315 320

Ser Ile Ile Glu Trp Ala Leu Ala Glu Met Ile Lys Asn Pro Ser Ile  
 325 330 335

Gln Lys Arg Ala His Gln Glu Met Asp Arg Val Ile Gly Arg Glu Arg  
 340 345 350

- 21 -

Arg Leu Leu Glu Ser Asp Ile Pro Asn Leu Pro Tyr Leu Lys Ala Ile  
355 360 365

Cys Lys Glu Ala Tyr Arg Lys His Pro Ser Thr Pro Leu Asn Leu Pro  
370 375 380

Arg Ile Ser Thr Asp Ala Cys Val Val Asp Gly Tyr His Ile Pro Lys  
385 390 395 400

Asn Thr Arg Leu Ser Val Asn Ile Trp Ala Ile Gly Arg Asp Pro Asp  
405 410 415

Val Trp Glu Asn Pro Leu Asp Phe Asn Pro Asp Arg Phe Met Ser Gly  
420 425 430

Leu Gln Gly Ile Glu Pro Gly Gly Asn His Phe Glu Leu Ile Pro Phe  
435 440 445

Gly Ala Gly Arg Arg Ile Cys Ala Gly Ser Arg Met Gly Ile Val Ile  
450 455 460

Val Glu Tyr Leu Leu Ala Thr Leu Val His Ser Phe Glu Trp Asp Leu  
465 470 475 480

Pro Ala Gly Ser Ala Glu Met Asp Met Glu Glu Val Phe Gly Leu Ala  
485 490 495

Leu Gln Lys Ala Val Pro Leu Ala Ala Arg Leu Thr Pro Arg Leu Pro  
500 505 510

Ser His Cys Tyr Ala Pro Pro Ser  
515 520

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<211> 1617  
<212> DNA  
<213> salvia

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ctctgcccc ggggccgagg ggctttccag tggtagggctc ccttcccttg ctgggcgaca 180  
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- 22 -

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<210> 16  
 <211> 518  
 <212> PRT  
 <213> salvia

<400> 16

Met Glu Ala Gln Glu Asn Met Leu Leu Ile Ala Arg Ala Leu Val Val  
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- 23 -

Ala Ser Leu Leu Tyr Ile Leu Ile Arg Met Phe Ile Ser Lys Leu Ser  
20 25 30

Thr Pro Gly His Pro Leu Pro Pro Gly Pro Arg Gly Phe Pro Val Val  
35 40 45

Gly Ser Leu Pro Leu Leu Gly Asp Met Pro His Val Ala Leu Ala Lys  
50 55 60

Met Ala Lys Thr Tyr Gly Pro Ile Met Tyr Leu Lys Met Gly Thr Val  
65 70 75 80

Gly Met Val Val Ala Ser Thr Pro Asp Ala Ala Arg Ala Phe Leu Lys  
85 90 95

Thr Gln Asp Ala Asn Phe Ser Asn Arg Pro Val Asn Ala Gly Ala Thr  
100 105 110

Ile Leu Ala Tyr Asn Ala Gln Asp Met Val Phe Ala Pro Tyr Gly Pro  
115 120 125

Lys Trp Arg Leu Leu Arg Lys Leu Ser Ser Leu His Met Leu Gly Ser  
130 135 140

Lys Ala Leu Glu Glu Trp Ala Asp Val Arg Thr Ser Glu Val Gly His  
145 150 155 160

Met Leu Ala Ala Met His Glu Ala Ser Arg Leu Asp Glu Ala Val Gly  
165 170 175

Leu Pro Glu Met Leu Val Tyr Ala Thr Ala Asn Met Ile Gly Lys Val  
180 185 190

Ile Leu Ser Arg Arg Val Phe Val Thr Lys Gly Lys Glu Met Asn Glu  
195 200 205

Phe Lys Glu Met Val Val Glu Leu Met Thr Thr Ala Gly Tyr Phe Asn  
210 215 220

Ile Gly Asp Phe Ile Pro Trp Leu Ala Trp Met Asp Leu Gln Gly Ile  
225 230 235 240

- 24 -

Glu Arg Gly Met Lys Lys Leu His Lys Lys Trp Asp Arg Leu Ile Gly  
245 250 255

Lys Met Leu Asp Asp Arg Leu Lys Ser Thr Tyr Lys Arg Asn Asp Lys  
260 265 270

Pro Asp Leu Leu Asp Ser Leu Leu Ala Asn His Asp Asp Glu Ser Lys  
275 280 285

Asp Asp Asp Glu Asp Cys Lys Leu Thr Thr Thr Asn Ile Lys Ala Leu  
290 295 300

Leu Leu Asn Leu Phe Thr Ala Gly Thr Asp Thr Ser Ser Ser Ile Ile  
305 310 315 320

Glu Trp Ala Leu Ala Glu Met Ile Lys Asn Pro Ser Ile Gln Lys Arg  
325 330 335

Ala His Gln Glu Met Asp Arg Val Ile Gly Arg Glu Arg Arg Leu Leu  
340 345 350

Glu Ser Asp Ile Pro Asn Leu Pro Tyr Leu Lys Ala Ile Cys Lys Glu  
355 360 365

Ala Tyr Arg Lys His Pro Ser Thr Pro Leu Asn Leu Pro Arg Ile Ser  
370 375 380

Thr Asp Ala Cys Val Val Asp Gly Tyr His Ile Pro Lys Asn Thr Arg  
385 390 395 400

Leu Ser Val Asn Ile Trp Ala Ile Gly Arg Asp Pro Asp Val Trp Glu  
405 410 415

Asn Pro Leu Asp Phe Asn Pro Asp Arg Phe Met Ser Gly Leu Gln Gly  
420 425 430

Ile Glu Pro Gly Gly Asn His Phe Glu Leu Ile Pro Phe Gly Ala Gly  
435 440 445

Arg Arg Ile Cys Ala Gly Ser Arg Met Gly Ile Val Ile Val Glu Tyr  
450 455 460



- 25 -

Leu Leu Ala Thr Leu Val His Ser Phe Glu Trp Asp Leu Pro Ala Gly  
 465 470 475 480

Ser Ala Glu Met Asp Met Glu Glu Val Phe Gly Leu Ala Leu Gln Lys  
 485 490 495

Ala Val Pro Leu Ala Ala Arg Leu Thr Pro Arg Leu Pro Ser His Cys  
 500 505 510

Tyr Ala Pro Pro Ser Ile  
 515

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 <211> 1730  
 <212> DNA  
 <213> sollya

<220>  
 <221> misc\_feature  
 <222> (1372)..(1372)  
 <223> n = any nucleotide

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 aagaccatgg cctattgtag gaaacctccc acaccttggc accaagccac accactccat 180  
 agctgccatg gctcggaat acgggtccct cctgcacctc cgcattgggca tcgtgcacgt 240  
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 aaaagcatat gatttcaaac aaatggtggt ggagctgatg actctagccg gtgagtttaa 660  
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 gaagaacgtg cacaatcgat tcgatgcgtt totgaatgta attttggagg agcataagct 780  
 gaaacttaat aatagtggac atggggaaca aaaacatatg gacttggtga gtacgttgat 840  
 tttgcttaag gatgatgctg atagtgaggg aggaaaactc actgatactg aaatcaaagc 900

- 26 -

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attagttggt catccaaagc ccagactaga ccatgaagtt tatcagtccc atggagttgt    1560
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<210> 18
<211> 521
<212> PRT
<213> sollya

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<400> 18

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Met Ala Thr Thr Leu Glu Phe Ile Leu Cys Phe Thr Ile Thr Ala Leu
1           5           10           15

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Pro Phe Leu Tyr Cys Ile Leu Asn Met Arg Ile Leu Leu Asn Arg His
20           25           30

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Pro Arg Ser Leu Pro Pro Gly Pro Arg Pro Trp Pro Ile Val Gly Asn
35           40           45

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Leu Pro His Leu Gly Thr Lys Pro His His Ser Ile Ala Ala Met Ala
50           55           60

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Arg Lys Tyr Gly Pro Leu Leu His Leu Arg Met Gly Ile Val His Val
65           70           75           80

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- 27 -

Val Val Ala Ala Ser Ala Asp Val Ala Ala Gln Phe Leu Lys Asn Asp  
85 90 95

Ala Asn Phe Ser Ser Arg Pro Pro Asn Ser Gly Ala Lys His Met Ala  
100 105 110

Tyr Asn Tyr His Asp Met Val Phe Ala Pro Tyr Gly Pro Arg Trp Arg  
115 120 125

Met Leu Arg Lys Ile Cys Ala Leu His Ile Phe Ser Ala Lys Ala Leu  
130 135 140

Asp Asp Phe His Arg Val Arg Glu Glu Glu Val Ala Ile Leu Ala Arg  
145 150 155 160

Thr Leu Ala His Ala Gly Gln Lys Pro Val Asn Leu Gly Gln Leu Phe  
165 170 175

Ser Thr Cys Asn Ala Asn Ala Leu Ser Val Leu Met Leu Gly Arg Arg  
180 185 190

Leu Phe Ser Thr Glu Val Asp Ser Lys Ala Tyr Asp Phe Lys Gln Met  
195 200 205

Val Val Glu Leu Met Thr Leu Ala Gly Glu Phe Asn Val Ser Asp Phe  
210 215 220

Ile Pro Pro Leu Glu Trp Leu Asp Leu Gln Gly Val Ala Ala Lys Met  
225 230 235 240

Lys Asn Val His Asn Arg Phe Asp Ala Phe Leu Asn Val Ile Leu Glu  
245 250 255

Glu His Lys Leu Lys Leu Asn Asn Ser Gly His Gly Glu Gln Lys His  
260 265 270

Met Asp Leu Leu Ser Thr Leu Ile Leu Leu Lys Asp Asp Ala Asp Ser  
275 280 285

Glu Gly Gly Lys Leu Thr Asp Thr Glu Ile Lys Ala Leu Leu Leu Asn  
290 295 300

- 28 -

Leu Phe Ser Ala Gly Thr Asp Thr Ser Ser Ser Thr Ile Glu Trp Val  
 305 310 315 320

Ile Ala Glu Leu Ile Arg Asn Pro Lys Ile Leu Ala Gln Ala Gln Arg  
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Glu Leu Asp Leu Val Val Gly Pro Asn Arg Leu Val Thr Asp Leu Asp  
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Asp Val Lys Gly Arg Asn Phe Glu Leu Ile Pro Phe Gly Ala Gly Arg  
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Ile Leu Ile Phe Leu Ile Thr His Leu Thr Ile His Ser Leu Phe Thr  
 20 25 30

Asn Arg His Lys Lys Leu Pro Pro Gly Pro Arg Gly Trp Pro Ile Val  
 35 40 45

Gly Ala Leu Pro Val Leu Gly Ser Met Pro His Val Thr Leu Ser Arg  
 50 55 60

Met Ala Lys Lys Tyr Gly Pro Val Met Tyr Leu Lys Met Gly Thr Lys  
 65 70 75 80

Asn Met Val Val Ala Ser Thr Pro Ala Ala Ala Arg Ala Phe Leu Lys  
 85 90 95

Thr Leu Asp Gln Asn Phe Ser Asn Arg Pro Pro Asn Ala Gly Ala Thr  
 100 105 110

His Leu Ala Tyr Asp Ser Gln Asp Met Val Phe Ala His Tyr Gly Ser  
 115 120 125

Arg Trp Arg Leu Leu Arg Lys Leu Ser Asn Leu His Met Leu Gly Gly  
 130 135 140

Lys Ala Leu Asp Asp Trp Ala His Val Arg Glu Lys Glu Met Arg Tyr  
 145 150 155 160

Met Leu Gly Ser Met Tyr Asp Cys Ser Lys Arg Gly Glu Ala Val Val  
 165 170 175

Val Ala Glu Met Leu Thr Tyr Ala Met Ala Asn Met Ile Gly Gln Val  
 180 185 190



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Ile Leu Ser Arg Arg Val Phe Glu Ser Lys Gly Ser Glu Ser Asn Glu  
 195 200 205

Phe Lys Asp Met Val Val Glu Leu Met Thr Val Ala Gly Tyr Phe Asn  
 210 215 220

Ile Gly Asp Phe Val Pro Phe Leu Ala Trp Phe Asp Leu Gln Gly Ile  
 225 230 235 240

Glu Arg Glu Met Lys Ala Leu His Lys Lys Phe Asp Ala Leu Leu Thr  
 245 250 255

Arg Met Ile Glu Glu His Val Ala Ser Arg Cys His Lys Gly Lys Gly  
 260 265 270

Asn Tyr Asp Phe Leu Asp Val Val Met Asp His Ser Ser Glu Ser Ser  
 275 280 285

Asp Gly Glu Arg Leu Thr Leu Thr Asn Val Lys Ala Leu Leu Leu Asn  
 290 295 300

Leu Phe Thr Ala Gly Thr Asp Thr Ser Ser Ser Val Ile Glu Trp Ala  
 305 310 315 320

Leu Ala Glu Met Leu Lys Asn Pro His Ile Thr Lys Arg Ala His Glu  
 325 330 335

Glu Met Asp Gln Val Ile Gly Lys Asp Arg Arg Leu Lys Glu Ser Asp  
 340 345 350

Leu Arg Asn Leu Pro Tyr Leu Gln Ala Ile Cys Lys Glu Ala Leu Arg  
 355 360 365

Lys His Pro Ser Thr Pro Leu Asn Leu Pro Arg Val Ser Ser Gln Pro  
 370 375 380

Cys Gln Val Asn Gly Tyr Tyr Ile Pro Lys Asn Thr Arg Leu Ser Val  
 385 390 395 400

Asn Ile Trp Ala Ile Gly Arg Asp Pro Glu Val Trp Glu Asn Pro Cys  
 405 410 415

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Glu Phe Asn Pro Glu Arg Phe Met Ser Gly Lys Gly Ala Lys Val Asp  
 420 425 430

Pro His Gly Asn Asp Phe Glu Leu Ile Pro Phe Gly Ala Gly Arg Arg  
 435 440 445

Val Cys Ala Gly Thr Arg Met Gly Ile Val Met Val Gln Tyr Ile Leu  
 450 455 460

Gly Thr Leu Val His Ser Phe Glu Trp Lys Leu Pro Asn Gly Val Val  
 465 470 475 480

Glu Leu Asn Met Glu Glu Thr Phe Gly Leu Ala Leu Gln Lys Lys Val  
 485 490 495

Pro Leu Ser Ala Leu Val Ser Pro Arg Leu His Pro Ser Ser Tyr Ile  
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Gln

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 <212> DNA  
 <213> chrysanthemum

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 cagctaccat tctagcgatc ggcaactgaa ctcgggctaa ttgtgtatat caagctgatt 180  
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 aatggggaca accaaaatct aaaatcacc acctaattct ctgcaccaca tctggtgtag 480  
 atatgcccgg ggctgattac caactacaa aactcctcgg cctcggccct tcggtcacac 540  
 gttttatgat gtaccaacaa ggggtgcttg cagggtggac ggttcttcgt ctagcaaaag 600  
 acctgcaga aaacaacaag gatgcacgtg tctagttgt ttgttcagag attactgcag 660  
 tcacattccg tggctcctaac gacactcacc ttgattcact cgttggtcaa gctttgtttg 720

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 <213> chrysanthemum

<400> 29

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Gln Gly Pro Ala Thr Ile Leu Ala Ile Gly Thr Ala Thr Pro Ala Asn
20           25           30

```

```

Cys Val Tyr Gln Ala Asp Tyr Pro Asp Tyr Tyr Phe Arg Ile Thr Lys
35           40           45

```

```

Ser Glu His Met Val Asp Leu Lys Glu Lys Phe Lys Arg Met Cys Asp
50           55           60

```

```

Lys Ser Met Ile Arg Lys Arg Tyr Met His Leu Thr Glu Glu Tyr Leu
65           70           75           80

```

```

Lys Glu Asn Pro Asn Leu Cys Glu Tyr Met Ala Pro Ser Leu Asp Ala
85           90           95

```

```

Arg Gln Asp Val Val Val Val Glu Val Pro Lys Leu Gly Lys Glu Ala
100          105          110

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- 44 -

Ala Thr Lys Ala Ile Lys Glu Trp Gly Gln Pro Lys Ser Lys Ile Thr  
115 120 125

His Leu Ile Phe Cys Thr Thr Ser Gly Val Asp Met Pro Gly Ala Asp  
130 135 140

Tyr Gln Leu Thr Lys Leu Leu Gly Leu Arg Pro Ser Val Lys Arg Phe  
145 150 155 160

Met Met Tyr Gln Gln Gly Cys Phe Ala Gly Gly Thr Val Leu Arg Leu  
165 170 175

Ala Lys Asp Leu Ala Glu Asn Asn Lys Asp Ala Arg Val Leu Val Val  
180 185 190

Cys Ser Glu Ile Thr Ala Val Thr Phe Arg Gly Pro Asn Asp Thr His  
195 200 205

Leu Asp Ser Leu Val Gly Gln Ala Leu Phe Gly Asp Gly Ala Ala Ala  
210 215 220

Val Ile Val Gly Ser Asp Pro Asp Leu Thr Lys Glu Arg Pro Leu Phe  
225 230 235 240

Glu Met Ile Ser Ala Ala Gln Thr Ile Leu Pro Asp Ser Glu Gly Ala  
245 250 255

Ile Asp Gly His Leu Arg Glu Val Gly Leu Thr Phe His Leu Leu Lys  
260 265 270

Asp Val Pro Gly Leu Ile Ser Lys Asn Ile Glu Lys Ala Leu Thr Gln  
275 280 285

Ala Phe Ser Pro Leu Gly Ile Ser Asp Trp Asn Ser Ile Phe Trp Ile  
290 295 300

Ala His Pro Gly Gly Pro Ala Ile Leu Asp Gln Val Glu Leu Lys Leu  
305 310 315 320

Gly Leu Lys Glu Glu Lys Met Arg Ala Thr Arg His Val Leu Ser Glu  
325 330 335

- 45 -

Tyr Gly Asn Met Ser Ser Ala Cys Val Leu Phe Ile Met Asp Glu Met  
340 345 350

Arg Lys Lys Ser Ala Glu Glu Gly Ala Ala Thr Thr Gly Glu Gly Leu  
355 360 365

Asp Trp Gly Val Leu Phe Gly Phe Gly Pro Gly Leu Thr Val Glu Thr  
370 375 380

Val Val Leu His Ser Leu Pro Thr Thr Val Ser Val Ala Asn  
385 390 395

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actgotagcc tagcttcttc catcttagcc caacaataga catcatttaa actagttggt 780  
ttaaacatgc taaccagcat aactatttcg tctttcaatc caccaatata caaactaata 840

- 46 -

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caattactac atttttatgt aatcatatct caatcaacag aattatgaga tgtggttgta	2580

- 47 -

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<213> lavendula

<400> 31  
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tcaccaccat taccacggc ggcagccacc gactgccgc agggccgagg ggctttccga 180  
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atttcacccc atggttgcct tggatggatt tgcaggggat agagagtggg atgaagaaat 780  
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atgcggagaa gctcacctca accaacgtca aggcctttt actgaacttg ttcaccgcag 960  
ggaccgacac gtcattcaagc ataatagaat gggcattggc cgagatgatc aagaatccaa 1020  
ccatcctaaa tagggcccac caagagatgg atagagtcgt tggtagaact cgaagggttg 1080

- 48 -

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<400> 32

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Ala Ala Ser Ile Tyr Phe Leu Ile Arg Tyr Phe Leu Ser Arg Ile Ile
20             25             30

```

```

Thr Thr Ile Thr His Gly Gly Ser His Arg Leu Pro Pro Gly Pro Arg
35             40             45

```

```

Gly Phe Pro Ile Val Gly Ala Leu Pro Leu Leu Gly Asp Met Pro His
50             55             60

```

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Val Ala Leu Ala Lys Met Ala Lys Thr Tyr Gly Pro Ile Ile Tyr Leu
65             70             75             80

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Lys Val Gly Ala Trp Gly Met Ala Val Ala Ser Thr Pro Ala Ser Ala
85             90             95

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- 49 -

Arg Ala Phe Leu Lys Thr Leu Asp Thr Asn Phe Ser Asp Arg Pro Pro  
 100 105 110

Asn Ala Gly Ala Thr Ile Leu Ala Tyr Asn Ala Glu Asp Met Val Phe  
 115 120 125

Ala Arg Tyr Gly Pro Lys Trp Arg Leu Leu Arg Lys Leu Thr Asn Leu  
 130 135 140

His Met Leu Gly Asn His Ala Leu Asp Gly Trp Ala Ser Val Arg Ser  
 145 150 155 160

Ser Glu Leu Gly Tyr Met Leu His Ala Arg His Asp Ala Thr Arg His  
 165 170 175

Gly Glu Pro Val Val Leu Pro Glu Met Leu Met Tyr Ala Val Gly Asn  
 180 185 190

Met Leu Gly Gln Val Ile Leu Ser Arg Arg Ile Phe Glu Lys Lys Gly  
 195 200 205

Lys Glu Val Asn Glu Leu Lys Asp Met Val Val Glu Leu Met Thr Ser  
 210 215 220

Ala Gly Tyr Phe Asn Ile Gly Asp Phe Ile Pro Trp Leu Ala Trp Met  
 225 230 235 240

Asp Leu Gln Gly Ile Glu Ser Gly Met Lys Lys Leu His Asn Lys Phe  
 245 250 255

Asp Lys Leu Ile Gly Lys Met Ile Glu Asp His Leu Lys Ser Ala His  
 260 265 270

Ile Arg Lys Ala Lys Pro Asp Leu Leu Asp Cys Leu Leu Ala Asn Arg  
 275 280 285

Asp Ser Ser Asp Ala Glu Lys Leu Thr Ser Thr Asn Val Lys Ala Leu  
 290 295 300

Leu Leu Asn Leu Phe Thr Ala Gly Thr Asp Thr Ser Ser Ser Ile Ile  
 305 310 315 320

Glu Trp Ala Leu Ala Glu Met Ile Lys Asn Pro Thr Ile Leu Asn Arg

- 50 -

325	330	335
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Glu Ser Asp Ile Pro Asn Leu Pro Tyr Leu Arg Ala Ile Cys Lys Glu 355 360 365		
Thr Tyr Arg Lys His Pro Ser Thr Pro Leu Asn Leu Pro Arg Ile Ala 370 375 380		
Ser Glu Pro Cys Val Val Asp Gly Tyr Tyr Ile Pro Lys Asn Thr Arg 385 390 395 400		
Leu Ser Val Asn Ile Trp Ala Ile Gly Arg Asp Pro Asp Val Trp Glu 405 410 415		
Asn Pro Leu Asp Phe Asn Pro Asp Arg Phe Leu Ser Gly Lys Asn Glu 420 425 430		
Arg Ile Asp Pro Arg Gly Asn His Phe Glu Leu Ile Pro Phe Gly Ala 435 440 445		
Gly Arg Arg Ile Cys Ala Gly Ala Arg Met Gly Met Val Leu Val Glu 450 455 460		
Tyr Ile Leu Gly Thr Leu Val His Ala Phe Glu Trp Glu Leu Pro Ala 465 470 475 480		
Gly Ala Gly Ala Gly Thr Ala Glu Leu Asn Met Asp His Val Phe Gly 485 490 495		
Leu Ala Leu Gln Lys Ala Val Pro Leu Thr Ala Met Leu Thr Pro Arg 500 505 510		
Leu Pro Ser His Cys Tyr Ala Pro 515 520		